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Sulzbacheromyces yunnanensis, a new record for Thailand

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Abstract—Specimens of a clavarioid basidiolichen collected in Thailand were identified as *Sulzbacheromyces yunnanensis*, based on morphology and similarities of ITS genes. A full description and illustration are provided. This is the first record of *S. yunnanensis* from Thailand

Key words—*Basidiomycota*, *Lepidostromataceae*, *Lepidostromatales*, Southeast Asia, taxonomy

Introduction

Sulzbacheromyces (*Lepidostromataceae*, *Lepidostromatales*) was described by Hodkinson & al. (2014) with *S. caatingae* (Sulzbacher & Lücking) B.P. Hodk. & Lücking as the type species. This genus is distributed in Africa, Asia and the neotropics. Eight species of *Sulzbacheromyces* have been described: *S. bicolor* D. Liu & al., *S. caatingae*, *S. chocoensis* Coca & al., *S. fossicola* (Corner) D. Liu & Li S. Wang, *S. miomboensis* De Kesel & Ertz, *S. sinensis*

(R.H. Petersen & M. Zang) D. Liu & Li S. Wang, *S. tutunendo* Coca & al., and *S. yunnanensis*. *Sulzbacheromyces* is characterized by clavarioid basidiomata combined with a lichenized crustose basal thallus with a chlorococcoid photobiont (Hodkinson & al. 2014, Sulzbacher & al. 2016, Liu & al. 2017, Coca & al. 2018).

Currently, only one *Sulzbacheromyces* species, *S. fossicola* has been reported from Thailand (Liu & al. 2017). During a survey of macrofungi collected in northeastern Thailand, we found specimens that corresponded to the description of *S. yunnanensis*, a species previously reported from China (Liu & al. 2017). Here we describe and illustrate the morphological characteristics of the Thai material and provide evidence of ITS gene sequence matches in GenBank.

Materials & methods

Morphology

Basidiomata were collected from the forest, Sisaket Province, Thailand, and kept in plastic collection boxes until transported back to the laboratory. Macroscopic descriptions of specimens were based on examination of fresh basidiomata. Ecological observations were recorded and photographs were taken in the field. Color names and codes follow Kornerup & Wanscher (1978). The specimens were dried at 40–45 °C in an electric food dryer. The micromorphological data were derived from dried specimens mounted in 95% ethanol and rehydrated in distilled water, 3% KOH, or Melzer's reagent. Dried specimens were deposited in the herbarium of Research Laboratory for Excellence in Sustainable Development of Biological Resources, Faculty of Science, Chiang Mai University, Thailand (SDBR-CMU).

DNA isolation, amplification, analyses

Genomic DNA was extracted from fresh material using a Favorgen DNA Extraction Mini Kit following the manufacturer's instructions. The internal transcribed spacer (ITS) region of ribosomal DNA (rDNA) was amplified by polymerase chain reaction (PCR) using ITS4 and ITS5 primers under the following thermal conditions: 94 °C for 2 min; 35 cycles of 95 °C for 30 s, 52 °C for 30 s, and 72 °C for 1 min; and 72 °C for 10 min. Negative controls lacking fungal DNA were run for checking any contamination of reagents. PCR products were checked on 1% agarose gels stained with ethidium bromide under UV light and purified using a Macherey-Nagel NucleoSpin Gel and PCR Clean-up Kit following the manufacturer's protocol. The purified PCR products were directly sequenced. Sanger sequencing was performed by 1ST Base Company (Kembangan, Malaysia) using the PCR primers cited above. Sequences were used to query GenBank database via BLAST (http://blast.ddbj.nig.ac.jp/top-e.html).

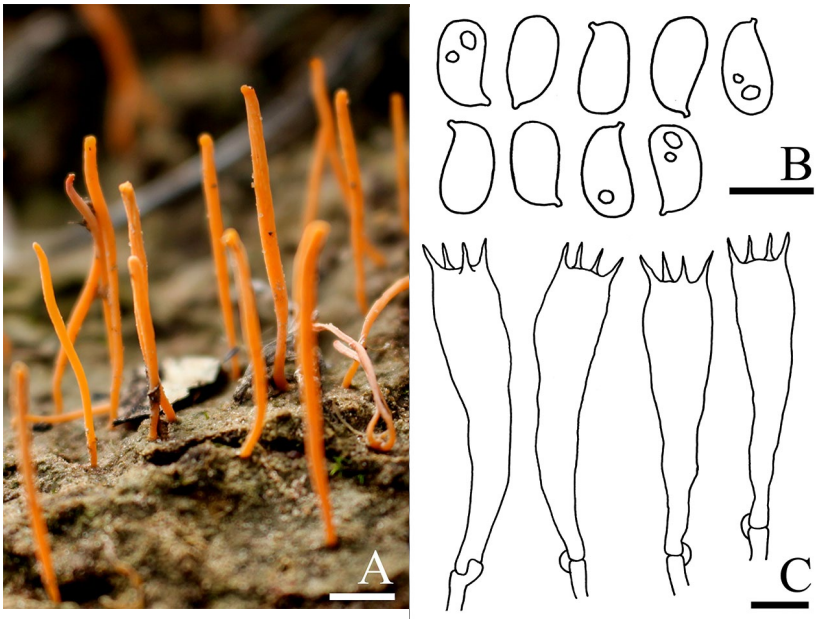

Fig. 1. *Sulzbacheromyces yunnanensis* (SDBR-CMU-NK0329).
A: basidiomata; B: basidiospores; C: basidia. Scale bars: A = 10 mm; B, C = 10 µm.

Sequence analysis

The ITS sequences of our Thai specimens were deposited in GenBank database as MK085985 and MK086016. Our ITS sequences were 100% similar to the *S. yunnanensis* KUN 14-44123 holotype sequence NR159026.

Taxonomy

Sulzbacheromyces yunnanensis D. Lui, Li S. Wang & Goffinet, Mycologia 109: 742 (2017). Fig. 1

Thallus crustose, covering an area of 0.5–50 mm diam., distinct and dark green when growing in shade or depressions, but yellow green and indistinguishable from soil when growing on exposed ground; forming a thin layer on the substrate, containing clusters of single-celled chlorococcoid algae, without prothallus. Photobiont chlorococcoid, 4–10 µm diam., globose to subglobose, smooth, contiguous, surrounded by a single layer of hyaline hyphae. Basidioma solid, clavarioid or cylindrical, fusiform or heliciform, simple (rarely once branched), with two conspicuous wide longitudinal

depressions or grooves, never circled by transverse cracks at maturity, apex obtuse to narrowly obtuse to truncate, 25–50 × 0.5–2.5 mm, with hymenium tissue covering the upper part; surface pruinose, without tomentum or mycelial patch at the base, orange-yellow (4A7) or light orange (6A4) when exposed to rain and direct sunshine, orange (6A6) in shaded habitat, base dark ochraceous, turning ochraceous overall upon drying. Trama hyphae 2–7 µm diam., parallel aligned, clamped, slightly thick-walled, densely agglutinated, with a bulbous apex. Hymenium 70–80 µm thick.

Basidiospores 8.5–12 × 3.5–5.8 µm (n = 50), Q = 2.0–2.4, ellipsoid to slightly reniform, thin-walled, hyaline, smooth, sometimes guttulate. Basidia 50–75 × 5–6.5 µm, oblong when young, subclavate to clavate when mature, thin-walled, hyaline, 4-spored, with basal clamp connections and sterigmata ≤5 µm long.

Specimens examined — **THAILAND**, **Sisaket Province**, **Khun Han District**, 14°52′20″N 104°38′01″E, elevation 208 m, on soil, 2 June 2018, Suwannarach N. & Kumla J. (SDBR-CMU-NK0329; GenBank MK085985); 3 June 2018, Suwannarach N. (SDBR-CMU-NK0342, GenBank MK086016).

Discussion

The clavarioid basidiomata, lichenized crustose basal thallus, and chlorococcoid photobiont support placement of our collections in *Sulzbacheromyces* (Hodkinson & al. 2014). The two specimens collected in northeastern Thailand were morphologically identified as *S. yunnanensis* based on the descriptions and keys in Liu & al. (2017). The orange-yellow to orange basidiomata of *S. yunnanensis* are similar to those of *S. caatingae*, *S. chocoensis*, *S. miomboensis*, *S. sinensis,* and *S. tutunendo*. However, the longer basidia of *S. yunnanensis* (50–75 µm) clearly distinguish this species from *S. caatingae* (23–45 µm), *S. chocoensis* (25–40 µm), *S. miomboensis* (21.1–30.3 µm), *S. sinensis* (15–50 µm), and *S. tutunendo* (25–40 µm) (Sulzbacher & al. 2016, Liu & al. 2017, Coca & al. 2018). The basidiospores of *S. caatingae* (5–8.5 µm), *S. chocoensis* (4 µm), and *S. tutunendo* (4 µm) (Sulzbacher & al. 2016, Coca & al. 2018) are clearly shorter than those of *S. yunnanensis* (8.5–12 µm). The ITS sequence matches in GenBank confirmed our two Thai specimens as *S. yunnanensis*, supporting the morphological identification (Coca & al. 2018).

Including our new record, four species of *Sulzbacheromyces* have been reported in Asia (Liu & al. 2017): *S. bicolor* in China; *S. fossicola* in China, India, Singapore, and Thailand; *S. sinensis* in China and Japan; and *S. yunnanensis* in China and Thailand. Of the four other *Sulzbacheromyces* species, three (*S. caatingae*, *S. chocoensis*, *S. tutunendo*) are known from the neotropics

(Brazil and Colombia; Sulzbacher & al. 2016, Coca & al. 2018), while *S. miomboensis* is known only from Africa (Democratic Republic of Congo; Liu & al. 2017).

The present study combining morphological characteristics and sequence data supports the identification of *S. yunnanensis* and a new record for Thailand.

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